

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH MUS MUSCULUS INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN SEQ IN NO:13

Query: IGFBP_like protein (SEQ ID NO: 6)

Subject: >gi|9055246 (AB006141) IGFBP-like protein [Mus musculus] SEQ ID NO: 13

Length = 270

Score = 1170 (416.9 bits), Expect = 1.8e-118, P = 1.8e-118
Identities = 209/269 (77%), Positives = 232/269 (86%)

Query:	8	LPLLLLLLLLLPPLSPSLGIRDVGRRPKGRCRPEGCPAPAPGIALDECGCCA	67
		+P L LLLL LLP L+ LG+RD G R P+C PC+ + CPAP+PCPAP ISA DECGCCA	
Sbjct:	1	MPRLPLLLL-LLPSLARGLGRLDAGRRHPECSPCQQRCPAPSPCPAPWISARDECGCCA	59
Query:	68	RCLGAEGASCGRAGRCGPGLVCASQAAGAAPEGTGLCVCAQRGTVCGSDGRSPSVCA	127
		RCLGAEGASCGG G RCGPGLVCAS+A+G APEGTGLCVCAQRG VCGSDGRSY S+CA	
Sbjct:	60	RCLGAEGASCGPGVSGRCGPGLVCASRASGTAPEGTGLCVCAQRGAVCGSDGRSYSSICA	119
Query:	128	LRLRARHTPRAHPGHLHKARDGCPCEFAPVVVPPRSVHNVTGAQVGLSCEVRAVTPVIT	187
		LRLRARH PRAH GHLHKARDGCPCEFAPVV++PPR +HNVTG QV LSCEV+AVPTPVIT	
Sbjct:	120	LRLRARHAPRAHHGHLHKARDGCPCEFAPVVLMPPRDIHNVTGTQVFLSCEVKAVTPVIT	179
Query:	188	WRKVTKSPEGTQALEELPGDHVNIQVVRGGPSDHEATAWILINPLRKEDEGVYQCHAAAN	247
		W+KV SPEGT+ LEELPGDHVNIQVVRGGPSDHE T+WILINPLRKEDEGVY CHAAAN	
Sbjct:	180	WKKVKHSPEGTEGLEELPGDHVNIQVVRGGPSDHETTSWILINPLRKEDEGVYHCHAAAN	239
Query:	248	MVGEAESHTVTVLDLSKYRSFHFAPDD	276
		+GEA+SH TTVTVDL++Y+S + P D	
Sbjct:	240	AIGEAQSHGTVTVLDLNRKSLYSVPGD	268

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH HOMO SAPIENS PROSTOGLANDIN I2 SEQ NO:14

Query: IGFBP_like protein (SEQ ID NO: 6)
 Subject: >gi|1082724 Prostaglandin I2 [Homo sapiens (SEQ ID NO: 14)]
 Length: 273

Score = 570 (205.7 bits), Expect = 7.9e-61, P = 7.9e-61
 Identities = 123/273 (45%), Positives = 150/273 (54%)

Query: 4 PSLRALLGAAGLLLLLLL--PLSSSS--SDT-----CGPCPASCPLPLGCLLGETR 54
 P L +LLL LLLL L PLS S D CGPC P CP P
 Sbjct: 2 PRL-SLLPLLLLLLLLPLPLSPSLGIRDVGRRPKCGPCRPEGCPAPAPCPAPGISAL 60

Query: 55 DACGCCPMARGEPEPCGGGAGRGYCAPMECVKSRKRKKGKAGAAAGPGVSGVCVK 114
 D CGCC C EG CGG GR C PG+ C AGAA G +G+CVC
 Sbjct: 61 DEGCCARCLGAEGASCGRAGGR--CGPGLVCASQA-----AGAAPEG---TGLCVCA 109

Query: 115 SRYPVCGSDGTTYPSCQLRAASQRAESRGEKAITQVSKGTCEQGPSIVTPPKDIWNVTG 174
 R VCGSDG +YPS C LR ++ + + G CE P +V PP+ + NVTG
 Sbjct: 110 QRGTVCGSDGRSYPSCALRLRARHTPRAHPGHLHKARDGCPCEFAFVVVPPRSVHNVTG 169

Query: 175 AQVYLSCEVIGIPTPVLWNKVKGHYGVQRTTELLPGDRDNLAIQTRGGPEKHEVTGWVL 234
 AQV LSCEV +PTPV+ W KV + G Q E LPGD N+A+Q RGGP HE T W+L
 Sbjct: 170 AQVGLSCEVRAVPTPVITWRKVTKSPEGTQALEELPGDHVNIQVVRGGPSDHEATAWIL 229

Query: 235 VSPLSKEDAGEYECHASNQSQASASAKITVVD 267
 ++PL KED G Y+CHA+N G+A + +TV+D
 Sbjct: 230 INPLRKEDEGVYQCHAAANMVGEAESHSTVTVLD 262

FIG. 2